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Timestamp: [year=2008; month=12; day=3; hr=15; min=26; sec=33; ms=357;]

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Application No: 10565183 Version No: 2.0

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No. of SeqIDs Defined: 8
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<110> Vermeij, Paul

<120> Hybrid Toxins Comprising Shiga-Like Toxin Subunits Fused to
Escherichia Coli Heat Labile Enterotoxin Subunits and Vaccines
Thereof

<130> 2003.006 US

<140> 10565183

<141> 2008-11-12

<150> PCT/EP04/51522

<151> 2004-07-16

<150> EP 03077266.9

<151> 2003-07-21

<160> 8

<170> PatentIn version 3.3

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<222> (1)..(954)

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ttt tct tcg gta tcc tat tcc cag gag ttt acg ata gac ttt tcg act	96
Phe Ser Ser Val Ser Tyr Ser Gln Glu Phe Thr Ile Asp Phe Ser Thr	
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caa caa agt tat gta tct tcg tta aat agt ata cgg aca gtg ata tcg	144
Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser	
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acc cct ctt gaa cat ata tct cag gga gct aca tcg gta tcc gtt att	192
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile	
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aat cat aca cca cca gga agt tat att tcc gta ggt ata cga ggg ctt	240
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu	
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gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga	288
Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg	
85 90 95	

aat aat tta tat gtg gct gga ttt gtt aat acg aca aca aat act ttc	336
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe	
100 105 110	
tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
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att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
130 135 140	
gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
145 150 155 160	
tca tat ctg gcg tta atg gag ttc agt ggt aat aca atg acc aga gat	528
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
165 170 175	
gca tca aga gca gtt ctg cgt ttt gtc act gtc aca gca gaa gcc tta	576
Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu	
180 185 190	
cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act	624
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr	
195 200 205	
gct cct gtt tat acg atg acg ccg gaa gac gtg gac ctc act ctg aac	672
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn	
210 215 220	
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Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly	
225 230 235 240	
gtc aga gtg ggg aga ata tcc ttt aat aat ata tca gcg ata ctt ggt	768
Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly	
245 250 255	
act gtg gcc gtt ata ctg aat tgt gga aat tca tca aga aca atc aca	816
Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr	
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ggt gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc	864
Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu	
275 280 285	
agg gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag	912
Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln	
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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser
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Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile
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Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg
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Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr
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Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala
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Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser
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Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp
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Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu
180 185 190

Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr
195 200 205

Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn
210 215 220

Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly
225 230 235 240

Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly
245 250 255

Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr
260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu
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gtatccgtta ttaatcatac accaccagga agttatatatt ccgtaggtat acgagggctt	240
gatgtttatc aggagcggtt tgaccatctt cgtctgatta ttgaacgaaa taatttatat	300
gtggctggat ttgttaatac gacaacaaat actttctaca gattttcaga ttttgacat	360
atatcattgc ccggtgtgac aactatttcc atgacaacgg acagcagtta taccactctg	420
caacgtgtcg cagcgctgga acgttccgga atgcaaata gtcgtcactc actggtttca	480
tcataatctgg cgtaaatgga gttcagtggg aatacaatga ccagagatgc atcaagagca	540
gttctgcgtt ttgtcactgt cacagcagaa gccttacggg tcaggcaaat acagagagaa	600
tttcgtctgg cactgtctga aactgctcct gtttatacga tgacgccgga agacgtggac	660
ctcactctga actgggggag aatcagcaat gtgcttccgg agtatcgggg agaggctggg	720
gtcagagtgg ggagaatatc ctttaataat atatcagcga tacttggtac tgtggccgtt	780
atactgaatt gtggaaattc atcaagaaca atcacaggtg atacttgtaa tgaggagacc	840
cagaatctga gcacaatata tctcaggga tatcaatcaa aagttaagag gcagatat	900
tcagactatc agtcagaggt tgacatatat aacagaattc gggatgaatt atg aat	956
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gca cac gga gct ccc cag act att aca gaa cta tgt tcg gaa tat cgc	1052
Ala His Gly Ala Pro Gln Thr Ile Thr Glu Leu Cys Ser Glu Tyr Arg	
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Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr Thr Glu	
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tcg atg gca ggc aaa aga gaa atg gtt atc att aca ttt aag agc ggc	1148
Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys Ser Gly	
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gaa aca ttt cag gtc gaa gtc ccg ggc agt caa cat ata gac tcc cag	1196
Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln	
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aaa aaa gcc att gaa agg atg aag gac aca tta aga atc aca tat ctg	1244
Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr Tyr Leu	
85 90 95	

acc gag acc aaa att gat aaa tta tgt gta tgg aat aat aaa acc ccc 1292
Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys Thr Pro
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Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
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Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
50 55 60

Ser Gly Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
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Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
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Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
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